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Spatiotemporal distribution of beluga stocks (*Delphinapterus leucas*) in and around Hudson Bay: Genetic mixture analysis based on mtDNA haplotypes

Répartition spatiotemporelle des stocks de bélugas (*Delphinapterus leucas*) à l'intérieur et autour de la baie d'Hudson : analyse du métissage génétique fondée sur les haplotypes d'ADNmt

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ABSTRACT

Stocks of belugas have been defined on the basis of summer aggregations in distinct areas. In the vicinity of Hudson Bay, the Western Hudson Bay (WHB), the Southeastern Baffin Island (SB), and the threatened Eastern Hudson Bay (EHB) stocks may contribute to the harvest by northern Nunavik communities. The contribution of the endangered Ungava Bay stock is also possible despite the very low census estimates for this population. Here, a genetic mixture analysis was performed with 37 mitochondrial haplotypes distributed among 1432 belugas caught in the Hudson Bay - Hudson Strait - Baffin Island geographical complex between 1984 and 2004. Genetic differentiation validated the traditional definition of beluga stocks in this area. The probabilistic estimation of stock contribution to mixed samples was heterogeneous among sectors and seasons. Contributions of the WHB and SB extended into Hudson Strait and Ungava Bay, but generally decreased further away from the summering grounds. Overall, the EHB stock contributed to an estimated 11 % of all mixed samples. EHB was best represented in spring and fall along the northeastern coast of Hudson Bay and in Ungava Bay, respectively. The array of haplotypes is unusual and very variable at Sanikiluaq, with the spring composition suggesting, as per other studies, a distinct, fluid population in the vicinity.

RÉSUMÉ

Les stocks de bélugas ont été déterminés sur la base de leur répartition estivale dans différentes zones. Les collectivités du Nunavik du Nord pêchent les stocks de l'ouest de la baie d'Hudson, du sud-est de le l'île de Baffin et de l'est de la baie d'Hudson (aujourd'hui menacés). La pêche du stock menacée de la baie d'Ungava se poursuit également en dépit des très faibles estimations de recensement de cette population. Une analyse du métissage génétique y a été menée avec 37 haplotypes mitochondriaux répartis chez 1432 bélugas capturés dans le complexe géographique baie d'Hudson - détroit d'Hudson - île Baffin entre 1984 et 2004. La différenciation génétique a validé la définition traditionnelle des stocks de bélugas dans la région. L'estimation probabiliste de la contribution du stock aux échantillons mixtes varie selon les régions et les saisons. Bien que les contributions de l'ouest de la baie d'Hudson et du sud-est de l'île Baffin se soient propagées au détroit d'Hudson et à la baie d'Ungava, elles décroissent généralement à l'écart des zones d'estivage. Le stock de l'est de la baie d'Hudson a contribué à environ 11 % de l'ensemble des échantillons mixtes. L'est de la baie d'Hudson était mieux représenté au printemps et à l'automne, suivi de la côte nord-est de la baie d'Hudson ainsi que de la baie d'Ungava, respectivement. La série d'haplotypes est plutôt inhabituelle et varie fortement à Sanikiluaq, et la composition enregistrée au printemps laisse à penser qu'une population distincte pourrait se trouver dans la région. Cette hypothèse est par ailleurs corroborée par d'autres études.

INTRODUCTION

The beluga (*Delphinapterus leucas*) is a toothed whale with a pan-Arctic distribution. In eastern Canada, they extend into Hudson Bay, with a disjunct population in the St. Lawrence River. Belugas are highly mobile individuals, but they are strongly associated with coastal areas during the summer. The locations of these summering grounds, along with behavioral, morphometric, and genetic characteristics, have been used to define management stocks (Donovan 1992). In and around Hudson Bay, five stocks are recognized: west Hudson Bay (WHB), east Hudson Bay (EHB), Ungava Bay (UB), Baffin Bay, and Southeast Baffin (SB).

In the mid-nineteen century, heavy commercial harvesting in Ungava Bay and along the eastern Hudson Bay arc (Francis 1977, Finley et al. 1982) initiated major demographic declines in the two Nunavik stocks. Population assessments in the early 1980s indicated that beluga numbers remained low, possibly due to the high subsistence harvests at that time (Breton-Provencher 1980; Finley et al. 1982). Conservation concerns led to implementation of management plans to limit subsistence harvests in 1986 through meetings with the Anguvigaq Hunters, Fishers and Trappers Association, and since then harvest levels have been limited by a management plan (e.g. Anon 1987). More recent assessments have confirmed that beluga numbers in these areas remain low (Hammill et al. 2004; Kingsley et al this meeting). Recently, the Canadian Committee on Species of Endangered Wildlife in Canada (COSEWIC) has classified eastern Hudson Bay and Ungava Bay beluga populations as 'Endangered' (http://www.sararegistry.gc.ca/document/default_e.cfm?documentID=410)

Early attempts to identify beluga whale stocks assumed that the management objective was to maintain viable populations of a species throughout its range (Reeves and Mitchell 1987). With this in mind, Reeves and Mitchell (1987) proposed that there are many different beluga whale stocks each distinguished by its tendency to home in summer on a particular estuary or complex of estuarine embayments and if this were the case, then summer populations should be conserved in Cumberland sound, eastern Hudson Bay, western Hudson Bay and Ungava Bay. The development of genetic methods identified differentiation, particularly among different summer aggregations of belugas from different regions of the Canadian Arctic (Brennin et al. 1997; Brown Gladden et al. 1997, Brown Gladden et al. 1999, De March and Maiers 2001, De March et al. 2002, De March and Postma 2003). These summering grounds comprised distinct, or unique, mitochondrial haplotypes and/or formed distinct haplotype assemblages. The strongest pattern, confirmed by all subsequent studies with larger datasets, have demonstrated that belugas caught in the summer along the coast of eastern Hudson Bay arc form a genetically distinct population. This EHB population is most related to the St. Lawrence River stock, and significantly differentiated from the two main stocks in the vicinity, i.e. the western Hudson Bay Stock and the Southeast Baffin Stock. Later studies have provided more detailed description of each stock composition by improving sampling sizes, and also analysed samples from areas where mixed stock harvesting was suspected (De March and Maiers 2001, De March et al. 2002, De March and Postma 2003). From this, it was shown that the northern Nunavik beluga whale fishery most probably comprise an important proportion (7-31%) of belugas from the EHB stock (De March and Maiers 2001). It has also been suggested that whales caught at Sanikiluaq were distinct from EHB stocks and that the haplotype composition was surprisingly similar to that of northern Hudson Bay or Foxe Basin. However, the small size of samples from many critical areas and the lack of seasonal information prevented firm conclusions on stock composition.

Given the seasonal migratory movement of belugas in and out of Hudson Bay and the demographic decline of EHB stock, there are concerns that northern Nunavik communities may

harvest a disproportionate and excessive number of belugas belonging to the threatened EBH beluga whale population. Indeed, belugas from EHB are bound to be part of the hunting catch during the spring and fall migration along Northeastern Hudson Bay, Hudson Strait, and possibly Ungava Bay. Also possible is the contribution of EHB population into other adjacent areas, namely Western Hudson Bay, Foxe Basin, Southeast Baffin Bay, and Sanikiluaq. In order to refine management, estimates of contributions of the principal beluga stocks to the harvest of Nunavik communities outside EHB arc are required. Should these contributions vary in time and space, these estimates could assist in defining specific hunting season and quotas for different sectors.

In spite of the above, there are still concerns from Nunavik hunters about the stock structure of beluga that are hunted in the coastal waters around northern Quebec. The addition of new samples allows the Hudson Bay stock complex to be re-examined. This report also focuses on estimating the contribution of distinct beluga stocks to the harvest of Nunavik sectors and surrounding communities. It provides a new seasonal and regional picture on these contributions by applying a Genetic Mixture Analysis that includes the three stocks that could contribute to the harvest in Northeastern Hudson Bay, Hudson Strait, and Ungava Bay. It also addresses the status of whales from Sanikiluaq.

MATERIAL AND METHODS

Dataset analyzed

The analysis was performed with 234 bp mtDNA D-loop haplotypes defined for 1432 belugas hunted in eastern Arctic Canada from 1982 and 2004. The dataset included 37 haplotypes. Half of the individuals (53.6%) bear the same haplotype (H02) and 26 haplotypes were represented by more than 2 individuals. Information on longer DNA segments defined as 'extended haplotypes' (De March and Maiers 2001) were disregarded given that considering a greater number of haplotypes only reduces the sample size for each haplotype, thus decreasing our ability to conduct probabilistic Genetic Mixture Analysis (GMA, see below).

Genetic Mixture Analysis (GMA)

Mixture analyses consists in estimating the proportion of individuals that different source (or reference) populations contribute to an admixed population composed of individuals from all or a subset of these source populations. Here, we used the maximum-likelihood genetic stock identification method implemented in the software SPAM version 3.7 (Debevec et al. 2000, Alaska Dept Fish & Game 2003). This method iteratively estimates individual posterior probability of population membership. Unlike individual assignment tests, this method does not allocate each individual from a mixed sample to one of the source populations. Instead, each individual is split and assigned to each source population in proportion to the probability that it belongs to that population. Mixed sample composition is then estimated as the sum of these fractional assignments. This approach is more accurate when all individual assignments can not be made with high confidence (Pella and Masuda, 2005, Manel et al. 2005). For example, suppose a haplotype is most frequent in a given stock, say S, but is also found at another location L. elsewhere. With categorical assignment, this individual is automatically allocated to stock S. However, while the rare occurrence of this haplotype can truly reflect the presence of an animal from stock S at site L, it could also reveal the low but effective frequency of this type at site L. In this case, GMA offers a valid alternative because it is only the sum of similarly unusual and improbable occurrences at site L that can amount to a non-negligible contribution

of stock S to L. The distribution of haplotypes among beluga stocks is particularly amenable to the application of this technique. Indeed, large samples from summering grounds clearly define stocks, and some haplotypes are much more frequent in one particular stock. However, there are very few strictly private haplotypes, such that many individual assignments are more or less uncertain.

The first step in the GMA is to define source populations. Here, each source population includes belugas hunted in 'summering areas' during the summer, i.e. in July or August (SA, Table 1). Following a previous study (De March and Postma 2003), the two principal SAs are the Western Hudson Bay West population (WHB, from Churchill to Arviat, N= 134) and the Eastern Hudson Bay arc population (EHB, from Inukjuak to Long Island, N= 200). Here, we also consider the Southeast Baffin population (SB, Pangnirtung and Iqaluit, N= 241; De March et al. 2002, De March and Postma 2003). The genetic distinctiveness of these SAs was appraised by X^2 testing as well as by estimating F_{st} with Arlequin v.2 (Scneider et al. 2000)

Belugas hunted outside SA, or in a SA but not in summer, were considered as mixed samples whose composition in terms of each SA was to be determined (Table 2, N = 857). Mixed samples were spatially and seasonally structured. They were divided into six sectors: Northern Hudson Bay (NHB, Chesterfield Inlet to Coral Harbour, plus Cape Dorset), Northeastern Hudson Bay (NeHB, Imilik to Ivujivik), Hudson Strait (HS, Saluit to Kangiqsujjuaq), Ungava Bay (UB, Quaqtaq to Kuujjuaq), SB (essentially Kimmirut), and Foxe Basin (FB, Igloolik, Hall Beach, and Repulse Bay). Belugas from Sanikiluaq (Belcher Is) were analyzed separately, while data from James Bay was insufficient (N = 7) and pooled with EHB. Seasons were defined as follows: May and June were considered spring, July and August summer, September to November fall, and December to April winter. Capture season was known for 76 % of the individuals. GMA was conducted on mixed samples from each sector and season with a minimal sample size of 10 individuals, per sector for all seasons pooled, as well as per season for all sectors pooled. Mixed samples from the Eastern Hudson Bay arc were not analyzed because there were too few samples collected in this area in spring or fall, and no winter samples were analyzed (N < 10).

RESULTS

MtDNA Genetic profile of summering areas (Table 1)

Twenty-eight haplotypes documented among 575 individuals were used to define summering area source populations (SA, Table 1). One haplotype (H02) was largely dominant in both WHB (66%) and SB (52%) while much less common in EHB (15%). For EHB, H07, H17 and H18 made up 79% of the total number of haplotypes and were either absent (H17) or rare in WHB and SB. Haplotype H05 was almost absent from EHB while being somewhat frequent in WHB (9%) and SB (6%). In SB, the sum of haplotypes H06, H11, H13, H22 amounted to 33% while these haplotypes were either very rare or absent from WHB and EHB. For WHB, the most discriminative haplotype was H20, contributing 8% while entirely absent from the two other summer grounds.

As per previous studies, EHB had, by far, the most distinct set of haplotypes. Although WHB and SB shared H02 as their dominant haplotype, SB had a more diversified distribution with four discriminative haplotypes against a single one for WHB.

The overall distribution of haplotypes among the three summering areas was significantly different. Based on Chi-square tests, the global P-value was practically zero (10^{-76}) while the pairwise P-values were $3.1x\ 10^{-33}$, $2\ x\ 10^{-9}$, $9\ x\ 10^{-54}$ for pairs (WHB, EHB), (WHB, SB) and (EHB, SB), respectively. These very low P values are strongly indicative of genetic differentiation, as measured by mtDNA, between the three summer grounds. This contention is confirmed by significant pairwise F_{st} values between summering area (EHB-WHB: 0.316, EHB-SB: 0.267; WHB-SB: 0.034, all $p < 0.0001$). Thus, it is biologically and statistically justified to use these samples as source samples for the GMA. Moreover, it seems that the stock definition can be extended to include the few individuals that are caught within summering areas but not during the summer. Indeed, when the total catch within each area of the summering grounds (including non-summer samples) are used as mixed samples, GMA does not reveal any contribution from any other stocks (> 99% of the contribution is attributed to each stock). This provides additional evidence that the delineation of the summering areas is biologically meaningful and that the areas are privately occupied by each of the three types. And so it seems that they are seldom used as traffic lanes during seasonal migrations.

Genetic composition of mixed samples (Table 3)

When all individuals from potentially mixed stock samples are considered, the relative contribution of each source population is estimated with confidence at 64% (s.e. = 3%) for WHB, 11% (s.e. = 1%) for EHB, and 23% for SB (s.e. = 3%). However, compositions are highly heterogeneous among sectors. The WHB stock contributes the greatest proportion of whales in all sectors, including Kimmirut, and is overtly dominant in areas closer to the summering ground, i.e. Foxe Basin (97%, s.e. = 4%) and Northern Hudson Bay (89%, s.e. = 6%). Besides its unexpected presence in Foxe Basin (see below, summer), the EHB stock is observed in significant proportion only in northern Nunavik, where its contribution varies between 15 % (s.e. = 4%) in Northeastern Hudson Bay and Ungava Bay and 21% (s.e. = 4%) in Hudson Strait. The SB stock also contributes to these sectors, with estimated representation diminishing with increasing distances from Southeast Baffin Island. Overall, the composition in stocks is polarized in sectors near summering grounds and mixed in areas near Hudson Strait.

The seasonal heterogeneity coupled with these spatial patterns is also worth considering. When all sectors are considered, WHB belugas once again account for the greatest proportion of whales. This trend, however, is much less apparent in springtime, when the contribution of the SB stock is very important (44%, s.e. = 11%). Meanwhile, when all sectors are considered, including SB (KIM), the proportion of belugas originating from EHB is relatively constant at ca. 10%, but varies from 12% to 22% in spring and fall, respectively, for Nunavik alone.

In the spring, the composition estimates varied widely between sectors, but all sectors were a mixture of at least two beluga stocks. In NeHB, a great majority of whales were contributed by WHB but the proportion of EHB whales was substantial (31%, s.e. = 13%), and SB individuals were absent. On both sides of Hudson Strait, 2/3 of the whales were contributed by SB, with a low proportion of EHB belugas present only along the coast of Nunavik. In Ungava Bay, WHB whales were most common (66%, s.e. = 20%), along with a clear contribution of SB. The EHB stock is probably absent in UB during the spring. In all, the WHB belugas have the broader spring range, but SB whales are also contributing an important share of the harvest. The EHB stock accounts for only 9% of all mixed spring sample, and is restricted to northeastern Nunavik, where it amounts to 12%.

In summer, mixed samples caught outside SA proper were analyzed for each sector but NeHB. Again, the contribution of stocks to each sector is highly variable. As expected, summer

hunts in sectors near summering areas (FB & NHB; Kimmirut) are mostly composed of whales from that area. Surprisingly, an estimated 19% (s.e. 10 %) of Foxe Basin specimens comes from the EHB summer ground, while EHB does not contribute to NHB in the summer. As was the case with the spring samples, Hudson Strait shows the most heterogeneous stock composition, with a non-negligible contribution from all three summering areas. The summer stock composition in Ungava Bay was based on few animals (N = 15) and seems to be a mixture of the WHB and the SB stocks, with very few if any EHB representatives. No unknown source is apparent in that sector, and there are no haplotypes specific to UB (Table 2). Interestingly, the SB contribution is growing along the west-to-east axis while contribution at FB is null. Overall, the WHB stock dominates in northwestern waters while SB belugas are well-represented around Hudson Strait. The overall EHB harvest is unchanged at 9% (s.e. = 3%).

During the fall, the WHB stock dominates in all sectors. Only WHB animals remain in Foxe Basin. Both NeHB and UB appear as mixtures of all three stocks, with WHB contributing most, but EHB also being well represented. SB belugas are present in all sectors except Foxe Basin, and their representation increases from west to east. Overall, the EHB belugas have the most variable distribution, with 18 % (s.e. = 6%) in NeHB and 28% (s.e. = 9%) in Ungava Bay, averaging 22% for Nunavik.

Composition of Sanikiluaq samples

Although also dominated by H02, the haplotype composition of the 152 whales caught at Sanikiluaq is unusual in that it comprises 6 haplotypes (H08, H16, H39, H42, H46, H57 and H58, N=14) unseen elsewhere. Also somewhat unexpected is the high proportion of H06 (11%), a haplotype found almost exclusively in SB. Many whales (14%) also bear haplotypes typical of EHB. Overall, contributions of WHB, EHB and SB population to Sanikiluaq harvest are estimated to 35% (s.e. = 10%), 14% (s.e. = 4%), and 44% (s.e = 9%). Unlike the other sectors, the mixture analysis identifies the contribution of an 'unknown' source for 7% of the specimens. Composition estimates vary with season and are estimated at 30% (s.e. = 11%), 4% (s.e. = 3%) and 60% (s.e. = 11%) in the spring for the WHB, EHB and SB components, respectively, while 6% are deemed of another, unknown origin. Summer estimates support the presence of the EHB stock at Sanikiluaq during this season (41%, s.e. = 14%) but are otherwise very imprecise. In the fall, most whales are from WHB (98%, s.e. = 1%).

DISCUSSION

The distribution of haplotypes included in this study is similar to what has previously been described with earlier, smaller datasets. Namely, this study confirms the distinct character of the EHB arc haplotype array, the presence of unique SB haplotypes, and the lower differentiation of whales summering in WHB (Brown Gladden et al. 1997, De March and Maiers 2001, De March and Postma 2003). The stable and constant differences among whales of different summering areas support the utilization of these units as reference populations. Likewise, this study once again unveils the peculiar haplotype assemblage of Sanikiluaq, a mixture of haplotypes typical of eastern Hudson Bay and haplotypes otherwise typical of Southeast Baffin or Western Arctic (H06, Brown Gladden et al. 1997), along with an unusual quantity of rare, unique haplotypes.

The nature of the results obtained in this study is different from that of previous analyses. First, by considering *all* potential source populations, GMA yields global estimates of source contribution for each mixed sample; in particular, the estimated contribution of SB belugas to Nunavik and Hudson Bay harvest represents new information. Second, the spatiotemporal

structure of the results allows a probabilistic analysis of beluga movements based on seasonal summering ground population distribution. Indeed, the relatively large variations in the summer ground composition estimates between mixed regional-seasonal samples support the existence of solid, albeit probabilistic, connections between the area where belugas spend time in summer and their whereabouts during the rest of the year. Although most haplotypes cannot be used to categorically allocate specimens to their most likely summering ground type, the presence of several exclusive or nearly exclusive haplotypes within each summer ground type makes it possible to allocate a significant proportion of specimens with a high level of confidence. At times, the trends detected with this discrete, traditional analysis helps cross-validating the general picture of beluga space occupation revealed by GMA.

1) Western Hudson Bay stock (WHB)

Except for Kimmirut, the WHB stock dominates the composition of mixed samples. In the spring, WHB belugas are found in the north-east sector of Hudson Bay (69%) and Ungava Bay (66%), and are less well represented among Hudson Strait samples (24%). In the summer, WHB specimens dominate in westerly sectors (NHB, FB, HS), they represent the third of the composition in Ungava Bay, but are few along the southern coast of Baffin Island (Kimmirut). In fall, it is still the dominant type in NHB while the only type to remain in Foxe Basin. Generally, it is dominant in all hunting fall areas but with a decreasing proportion towards the east.

2) South Baffin stock (SB)

SB belugas do not seem to venture much into Hudson Bay. In springtime, however, SB specimens enter Hudson Strait and Ungava Bay and they contribute substantially to the mixed-stock harvest in this region (Hudson Strait: 65%, s.e. = 17%; Ungava Bay: 32%, s.e. = 19%). In summer, their representation decreases with distance from Baffin Island. In fall, SB specimens are still found in the northernmost sector of Hudson Bay. By then, their representation among the Ungava Bay samples has drastically decreased from 60% to an estimated 20%. SB whales, then, appear to intermingle with other stocks principally in the spring, in and near Hudson Strait.

3) Eastern Hudson Bay arc stock (EHB)

In springtime, EHB belugas are found mainly in Hudson Strait and along the northeastern coast of Hudson Bay. This result suggests a particularly early entrance of EHB in Hudson Bay, as they apparently contribute to 31% (s.e. = 13%) of the catch while representing ca. 5 % of the census population of Hudson Bay (Richard 2005; Hammill et al. 2004). In summer, when not in summering areas, EHB belugas may still be caught in Hudson Strait (12%, s.e. 7%) while being conspicuously absent in northern Hudson Bay and probably so in Ungava Bay. In Foxe Basin, belugas from EHB are reported in the summer harvest (19%). It appears, then, as had been observed in the past (Brown Gladden et al. 1997, De March et al. 2002), that some EHB specimens may stray in remote waters. This interpretation is supported by the low but sustained presence of haplotype typical of EHB (H07 and H18) at Repulse Bay and Hall Beach from 1994 to 2002. In summer, EHB belugas are also present near Sanikiluaq. In fall, EBH whales are again contributing a relatively large share of the harvest along northeastern Hudson Bay and Ungava, while data are insufficient to estimate the contribution of this stock to Hudson Strait harvest. When only Nunavik sectors are considered, EHB contribution is lower in the spring (12%) than in the fall (22%).

Overall, our estimates for EHB contribution to the mixed harvest over northern Nunavik communities (NeHB and UB: 15%; HS: 21%, Table 3) are lower than those provided by

DeMarch and Maiers (2001) (NeHB and HS: 31%) and close to those of De March and Postma (2003) (HS and UB: 19%, NeHB: 15%). However, we found no evidence whatsoever for a contribution of EHB to Northern Hudson Bay or Kimmirut catch. This contradicts previous estimations reaching 9-11% and 5-8%, respectively (De March and Maiers 2001, De March and Postma 2003). We feel that our estimates are more reliable because they rely on a larger dataset that included all potential sources, and, more importantly, on a method overcoming the problems associated with the unreliable assignment of haplotypes shared among summering areas.

4) Sanikiluaq

The peculiar genetic composition at Sanikuluaq is perfectly in line with what has been observed in the past, namely the presence of EHB haplotypes, along with haplotypes typical of northern Hudson Bay and a suite of rare, unique haplotypes (De March and Maiers 2001). The contribution of the nearby EHB stock seems undeniable, especially in the summer, when nearly a third of the whales bear haplotypes typical (H18) or unique (H17) to this stock (Table 2). The overall contribution of the EHB stock to Sanikiluaq, however, may be closer to 14% (s.e. = 4%). With regards to the presence of SB haplotypes in Sanikuluaq, the results and interpretation of the Genetic Mixture Analysis presented above strongly indicate that their heavy representation is unlikely to originate from the presence of the SB stock as far into Hudson Bay. Indeed, mixture analyses indicate that SB belugas are well represented in Hudson Strait but also that they are restricted to northern parts of Hudson Bay. It is thus very improbable that genuine representatives of the SB population are present at Sanikiluaq. This is especially true in the spring season, when haplotype H06, typical of SB, accounts for 18% of the available samples. Along with the presence of many unique haplotypes and evidence of an unknown source, the available data strongly argue for the existence of a distinct group of whales spending a significant proportion of the year near Sanikiluaq, most likely in spring. This population may have originated in part from northern whales and now be currently demographically disconnected from the current SB stock. Observations of belugas in the vicinity during winter, while Hudson Bay is mostly frozen, suggests that whales may overwinter in this area (Richard 1993, Lewis et al, 2009). However, the correspondence with the putative Sanikuluaq population remains elusive, because other stocks, and certainly EHB whales, are found in this area in the summer. Likewise, there is currently too little (genetic) information about whales from James Bay to evaluate if animals from the southernmost regions of Hudson Bay form a cohesive and distinct population. Genetic data from these areas are clearly needed.

Summary and perspectives

Three summering grounds (WHB, EHB, SB) were found to be significantly differentiated on the basis of the distribution of twenty-eight haplotypes. Significant connections were observed between the three summer ground types and spatiotemporal occupation within the Hudson Bay - Hudson Strait - Baffin Island geographical complex. Hudson Strait was the only sector to show concomitant occupation of the three types at any time. WHB stock is clearly the best represented stock in the dataset analyzed. EHB belugas are practically absent from the northern sector of Hudson Bay and they shared little space with SB belugas, except in Hudson Strait. SB belugas are well represented in that area but they do not contribute much to samples caught in Hudson Bay proper.

Overall, the EHB stock accounts for 11% of the mixed samples analyzed. However, unlike other analyses (De March and Maiers 2001), it is absent from NHB and Kimmirut. It is also

poorly represented in Ungava Bay, except in the fall. It is noticeably over-represented in the spring, and possibly in the fall, along the coast of northeastern Hudson Bay.

A proportion of whales near Sanikuluaq are certainly of an unusual, and variable, genetic composition. They may well form a distinct population that seasonally intermingles with other stocks, in particular with EHB whales during the summer. No evidence was found for the endangered Ungava Bay stock.

This study provides a new, complementary picture of stock composition in and around Hudson Bay. Unlike other studies, we considered all three stocks from the study area, and we proceeded to a probabilistic analysis relying on genetic mixture analysis. Our conclusions are in line with those of previous studies, but GMA allowed using smaller subsets of data, namely those of specific sectors in specific seasons.

The quality of the results and interpretation are contingent upon the identification and use of all potential source populations. We confirmed and validated the use of summering areas as source populations, but in the end we raised the possibility that Sanikiluaq may represent another population. However, at this stage and with the data available, it seems premature to consider Sanikiluaq as a potential source, especially because of the apparent seasonal variation in stock composition and the mix with EHB in the summer. Notwithstanding these arguments, an improved dataset with more data from whales taken in this general area in all seasons may, once available, justify considering this area as a potential source.

Another important analytical nuance is that the mixture analysis performed by SPAM can inflate lower estimates. We feel that the bias does not affect our interpretation of the data too severely because we have always considered standard errors on the mean estimated proportions. These errors are always relatively larger for small proportions, and we have taken care to indicate that some estimates may be null when appropriate. In the context of management, this potential bias could assist in applying the precautionary principle. In any cases, when using these estimated proportions to potentially define quotas, it is recommended that this bias be taken into consideration.

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Figure 1: General map with names of places and communities where belugas were captured and genotyped (From DeMarch and Postma, ResDoc 2001/050)

Table 1 : Occurrence of haplotypes in each belugas summering areas

Haplotype	Western Hudson Bay (WHB)	Eastern Hudson Bay (EHB)	Southeast Baffin (SB)	Total
H01			1	1
H02	88	29	125	242
H03			4	4
H04			1	1
H05	12	2	14	28
H06	2	1	18	21
H07	2	17	5	24
H11			11	11
H13			19	19
H17		24		24
H18	6	113	3	122
H19		2		2
H20	11			11
H21	1			1
H22	3		31	34
H23	3		2	5
H24			5	5
H26		2		2
H32	1	3	1	5
H35			1	1
H44	1			1
H45		1		1
H56	1			1
H59	2			2
H61		4		4
H63		1		1
H64	1			1
H67		1		1
Total	134	200	241	575

Table 2: **Distribution of mitochondrial haplotypes among samples from different sectors (FB: Foxe Basin; NHB: Northern Hudson Bay; NeHB: Northeastern Hudson Bay; HS (QC): Hudson Strait, Quebec; UB: Ungava Bay; SB(KIM): Southeast Baffin, Kimmirut) and taken in different seasons (Spring: May-June; Summer: July-August; Fall:September-November; Winter: December to April)**

		Haplotype																									
Sector	**Season**	H02	H04	H05	H06	H07	H08	H16	H17	H18	H20	H21	H22	H23	H24	H32	H35	H39	H42	H44	H46	H53	H55	H57	H58	H59	H63	**Total**
FB	Summer	11		1		1				5	8																	26
	Fall	27								1	10	1								1								40
	Unknown	7																										7
	Total	**45**		**1**		**1**				**6**	**18**	**1**								**1**								**73**
NHB	Summer	30		10						2	3		4	3			1									1		54
	Fall	37	1	7		1				2	1	2	4	2		1				1								59
	Unknown	11		1						2	1			1														16
	Total	**78**	**1**	**18**		**1**				**6**	**5**	**2**	**8**	**6**		**1**	**1**			**1**						**1**		**129**
EHB	Summer					1																	1				2	4
	Fall	5																										5
	Total	**5**				**1**																	**1**				**2**	**9**
NeHB	Spring	15		1		2				5																		23
	Summer	1				1																						2
	Fall	52	1	2		2			5	6		2	1				1					1						73
	Unknown	43	1	1	1				3		1		1										2					53
	Total	**111**	**2**	**4**	**1**	**5**			**8**	**11**	**1**	**2**	**2**				**1**					**1**	**2**					**151**
SAN	Spring	40			13	1	1	1	2		1	3					5	4										71
	Summer	10			1				4	2									1		1							19
	Fall	13				1																						14
	Winter	2								2																		6
	Unknown	24			2	3			1	5					2						2			1	1			42
	Total	**89**			**16**	**5**	**1**	**1**	**7**	**9**	**1**	**3**			**2**		**5**	**4**	**1**		**6**			**1**	**1**			**152**
HS(QC)	Spring	24	3	2	1	4				3		1	3		1		1											43
	Summer	24	1	2					1	4	3		3		1													39
	Fall					1			3	2	1																	7
	Winter	1																										1
	Unknown	30		3		6			2	7	2		2		1							2						55
	Total	**79**	**4**	**7**	**1**	**11**			**6**	**16**	**6**	**1**	**8**		**3**		**1**					**2**						**145**
UB	Spring	20			1	2				1	2						2											28
	Summer	9	1	2						1			2															15
	Fall	23	2	5		1			5	4																		40
	Unknown	23	3			3			1	1	1			1		1												34
	Total	**75**	**6**	**7**	**1**	**6**			**6**	**7**	**3**		**2**	**1**		**1**	**2**											**117**
SB(KIM)	Spring	12		2									3	1	1													19
	Summer	5											1		1													7
	Fall	28		13						2			7															50
	Winter	2																										2
	Unknown	2											1															3
	Total	**49**		**15**						**2**			**12**	**1**	**2**													**81**
Total		**531**	**13**	**52**	**19**	**30**	**1**	**1**	**27**	**57**	**34**	**9**	**32**	**8**	**7**	**2**	**10**	**4**	**1**	**2**	**6**	**3**	**3**	**1**	**1**	**1**	**2**	**857**

Table 3 **Estimated proportion of each stock of beluga (Source: WHB: Western Hudson Bay; EBH: Eastern Hudson Bay; SB: Southeast Baffin) in potetntially mixed samples from different sectors (FB: Foxe Basin; NHB: Northern Hudson Bay; NeHB: Northeastern Hudson Bay; HS (QC): Hudson Strait, Quebec; UB: Ungava Bay; SB(KIM): Southeast Baffin, Kimmirut).**

		Sector						
Season	**Source**	**FB**	**NHB**	**NeHB**	**HS (QC)**	**UB**	**SB(KIM)**	**All sector[1]**
	WHB	*	*	69 (13)	24 (17)	66 (19)	37 (33)	46 (12)
	EHB	*	*	31 (13)	10 (7)	2 (7)	0	9 (4)
Spring	**SB**	*	*	0	65 (17)	32 (19)	63 (33)	44 (11)
	Unknown			0	0	0		0
	N	*	*	23	43	28	19	113
	H	*	*	4	10	6	*	12
	WHB	81 (10)	86 (10)	*	60 (15)	34 (40)	9 (18)	72 (7)
	EHB	19 (10)	0	*	12 (7)	4 (9)	0	9 (3)
Summer	**SB**	0	14 (10)	*	28 (14)	61 (37)	91 (18)	19 (6)
	Unknown	0.7	0		0	0	0	0.7
	N	26	54	*	39	15	7	147
	H	5	8	*	8	5	3	14
	WHB	100 (<0.2)	86 (10)	67 (10)	*	52 (15)	70 (18)	77 (5)
	EHB	0	0	18 (6)	*	28 (9)	0	12 (2)
Fall	**SB**	0	14 (10)	13 (8)	*	20 (14)	30 (18)	11 (4)
	Unknown	0	0	1.4		0		0.4
	N	40	59	73	*	40	50	274
	H	5	11	10	*	6	*	14
	WHB	97 (4)	89 (6)	71 (7)	46 (8)	53 (10)	52 (15)	64 (3)
	EHB	3 (4)	0	15 (4)	21 (4)	15 (4)	0	11 (1)
All Seasons[1]	**SB**	0	11 (6)	11 (6)	32 (8)	31 (9)	48 (15)	23 (3)
	Unknown	0	0	2	1			2
	N	73	129	151	145	117	81	857
	H	7	14	13	13	12	14	26

[1] sample sizes of 'All Sectors'/ 'All Seasons' may exceed the sum of sample sizes per sector/season because some haplotypes were too few within sector/season to use in calculation

estimates < 0.1% are given a null (0)